

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: December 11, 2000, 10:23:53 : Search time 8511.27 Seconds  
(without alignments)  
348.684 Million cell updates/sec

Title: US-09-270-910-36

Perfect score: 480

Sequence: 1 ggigtgttaattatgagac.....actccagatgcctaacactaa 480

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 7189864 seqs, 3091403243 residues

Total number of hits satisfying chosen parameters: 14379728

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*  
10: gb\_est10: \*  
11: gb\_est11: \*  
12: gb\_est12: \*  
13: gb\_est13: \*  
14: gb\_est14: \*  
15: gb\_est15: \*  
16: gb\_est16: \*  
17: gb\_est17: \*  
18: gb\_est18: \*  
19: gb\_est19: \*  
20: gb\_est20: \*  
21: gb\_est21: \*  
22: gb\_est22: \*  
23: gb\_est23: \*  
24: gb\_est24: \*  
25: gb\_est25: \*  
26: gb\_est26: \*  
27: gb\_est27: \*  
28: gb\_est28: \*  
29: gb\_est29: \*  
30: gb\_est30: \*  
31: gb\_est31: \*  
32: gb\_est32: \*  
33: gb\_est33: \*  
34: gb\_est34: \*  
35: gb\_est35: \*  
36: gb\_est36: \*  
37: gb\_est37: \*  
38: gb\_est38: \*  
39: gb\_est39: \*  
40: gb\_est40: \*  
41: em\_estba: \*  
42: em\_estfun: \*  
43: em\_esthum1: \*  
44: em\_esthum2: \*  
45: em\_esthum3: \*  
46: em\_esthum4: \*  
47: em\_esthum5: \*  
48: em\_esthum6: \*  
49: em\_esthum7: \*  
50: em\_esthum8: \*  
51: em\_esthum9: \*  
52: em\_esthum10: \*  
53: em\_esthum11: \*  
54: em\_esthum12: \*  
55: em\_esthum13: \*  
56: em\_esthum14: \*  
57: em\_esthum15: \*  
58: em\_esthum16: \*  
59: em\_esthum17: \*  
60: em\_esthum18: \*  
61: em\_esthum19: \*  
62: em\_esthum20: \*  
63: em\_estin1: \*  
64: em\_estin2: \*  
65: em\_estin3: \*  
66: em\_estin4: \*  
67: em\_estom: \*  
68: em\_estrov1: \*  
69: em\_estrov2: \*  
70: em\_estp11: \*  
71: em\_estp12: \*  
72: em\_estp13: \*  
73: em\_estp14: \*  
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79: em\_estrov5: \*  
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84: em\_estrov10: \*  
85: em\_estrov11: \*  
86: em\_estrov12: \*  
87: em\_estrov13: \*  
88: gb\_gss1: \*  
89: gb\_gss2: \*  
90: gb\_gss3: \*  
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93: em\_gss2: \*  
94: em\_gss3: \*  
95: em\_gss4: \*  
96: gb\_gss5: \*  
97: gb\_gss6: \*  
98: gb\_gss7: \*  
99: gb\_gss8: \*  
100: gb\_gss9: \*  
101: em\_gss5: \*  
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103: em\_gss7: \*  
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106: em\_gss10: \*  
107: em\_gss11: \*  
108: gb\_gss10: \*  
109: gb\_gss11: \*  
110: em\_gss12: \*  
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112: gb\_gss13: \*  
113: gb\_gss14: \*  
114: gb\_gss15: \*  
115: gb\_gss16: \*  
116: gb\_gss17: \*



```

Db      490 GATGCTTTTCAAGCGGTGAGGTTACGTTTGGCCACCCGATTACAACTA 545
RESULT  2
LOCUS   AW782077
DEFINITION sm01b05.y1 Gm-c1027 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1027-7594 5' similar to TR:P93333 P93333 PR10-1 PROTEIN. [2]
TR:043350 ; mRNA sequence.
ACCESSION AW782077
VERSION   AW782077
KEYWORDS  EST.
SOURCE    soybean.
ORGANISM  Glycine max
           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
           Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
           Fabales; Fabaceae; Papilionoideae; Glycine.
REFERENCE 1 (bases 1 to 536)
AUTHORS   Shoemaker,R., Keim,P., Vodkin,L., Eprelding,J., Corryell,V., Khanna,
           A., Bolla,B., Marra,M., Haller,L., Kucaba,T., Martin,J., Beck,C.,
           Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,
           Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,
           R., Rittler,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,
           R., Mesterston,R. and Wilson,R.
           Public Soybean EST Project
           Unpublished (1999)
TITLE      Shoemaker R/Public Soybean EST Project
JOURNAL    Public Soybean EST Project
COMMENT    Washington University School of Medicine
           4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
           Tel: 314 286 1800
           Fax: 314 286 1810
           Email: estewatson.wustl.edu
           This clone is available through: Genome Systems, Inc. 4633 World
           Parkway Circle St. Louis, Missouri 63134 For further information
           call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
           427-3324 or contact: clones@genomesystems.com or
           info@genomesystems.com web site: www.genomesystems.com
           High quality sequence stop: 412.
           Location/Qualifiers
             1..536
               /organism="Glycine max"
               /db_xref="taxon:3847"
               /clone="GENOME SYSTEMS CLONE ID: Gm-c1027-7594"
               /clone_1ib="Gm-c1027"
               /tissue_type="cotyledons of 3- and 7-day-old Williams
               seedlings"
               /lab_host="DH10B"
               /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
               XhoI; This cDNA library was constructed from mRNA isolated
               from cotyledons of 3- and 7-day-old Williams seedlings
               which were propagated on paper towels with distilled
               water. The cotyledons were flash-frozen in liquid
               nitrogen, then lyophilized for 72 hours. Unequal amounts
               of mRNA was used for cDNA synthesis. Stratagene's cDNA
               Synthesis Kit (catalog number 200401) was used to
               synthesize the cDNA. First-stranded synthesis was
               performed with 5-methyl dCTP, hence the ligated cDNA was
               hemimethylated. A modification of Stratagene's
               first-strand synthesis primer was used. An anchor
               nucleotide (V-A, C, or G) was added to the 3' end of the
               primer (GAGAGAGAGAGAGAGAGACAGTCAG(T)18) to anchor
               the primer at the 5' end of the poly(A) tract. After
               second-strand synthesis, the cDNA ends were filled in
               with cloned pfu DNA, ligated to EcoRI adapters and
               subsequently phosphorylated. The XhoI site within the
               first-strand synthesis primer was then restricted by
               digestion with XhoI; all XhoI sites in the cDNA would be
               protected by their hemimethylated status. The cDNA
               constructs were size-fractionated with a 500 bp cutoff,
               using G130BRL Life Technologies' cDNA Size Fractionation
               column. The column eluent was then ligated into

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Stratagene's pBluescript(tm) II XR Predigested vector
(pBluescript II SK(+)) that has been digested with EcoRI
and XhoI, and phosphorylated by Stratagene). 97% of the
white and blue colonies appear to contain recombinant
plasmids with cDNA inserts, based on size (n=30). This
library was constructed by Dr. Paul Keim and Dr. Virginia
Corryell.
BASE COUNT 150 a 121 c 113 g 151 t 1 others
ORIGIN
Query Match      35.6%; Score 171; DB 24; Length 536;
Best Local Similarity 61.8%; Pred. No. 1,le-39;
Matches 289; Conservative 0; Mismatches 176; Indels 3; Gaps 1;
Oy      1 ggtgtttaatatatagactgagaccacctctgtatcccaagcagctgcagtcgaag 60
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      69 ggtgttttactcagattatattatgattaccctgcgtgcgtctccttctgagcattcama 128
Oy      61 gctttatcccttgatgagcagatacctcttccaaaggttgacacccaagccattagcagt 120
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      129 gccatgacattagatttccatatacctcttccaaagccttgctg--ATAGCATCCACAGC 185
Oy      121 gttgaacaattgaaagaaatgagggccttgagaccattaaagagatgacttcccgaa 180
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      186 attgtttttaccccaagaaatggtgtcttgcgacacatcacaagaatccattgaa 245
Oy      181 ggcctcccttcaagtaagcagagacagatgattgaggtgagacacaacaattcaaa 240
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      246 gctgacaaaacagatattgctgcacacagattgattgattgattgattgattgattgatt 305
Oy      241 tacaattacagcgtgatcgaggcggttcccatagcgcacacattgagaagatctccaac 300
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      306 tatmaacttgcagatattctgagggcactgcttgcctgacacattggagagaggtcttatttc 365
Oy      301 gagataaagatagtggaaccccttgatgagatcatcttgatgaatcgcaacaagttac 360
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      366 gaagcccaattggtgtgagagctccaattggaggtccatttanganagattagttgcagatt 425
Oy      361 cacaccaaaagtgaccatagtgatgaaagcagagcagattaaagcaagtaagaagatgggc 420
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      426 ttacacaaaaggcagatctgacgttactgagagagactctacccaacaaagccaaagatc 485
Oy      421 gagacactttgagggcgttgagagactacctcttgacacactcgat 468
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      486 caagcgcttgaagacttgaagggttacttggcaaatctgatt 533
RESULT  3
LOCUS   AW980848
DEFINITION EST392001 GVN Medicago truncatula cDNA clone gcvn-58L14, mRNA
sequence.
ACCESSION AW980848
VERSION   AW980848
KEYWORDS  EST.
SOURCE    Medicago truncatula
           Medicago truncatula
           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
           Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
           Fabales; Fabaceae; Papilionoideae; Medicago.
REFERENCE 1 (bases 1 to 698)
AUTHORS   Fedorova,M., Peterson,B.L., Samac,D.A., Vance,C.P., Gantt,J.S., Peng,
           H., Ellis,L., Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S.,
           Holt,I.E. and Fraser,C.M.
           ESTs from one month old nitrogen-fixing root nodules of Medicago
           truncatula
           Unpublished (2000)
           Contact: Carroll P. Vance
           Department of Agronomy and Plant Genetics
           University of Minnesota
           411 Borlaug Hall, 1991 Upper Buford Circle, St. Paul, MN 55108 USA
           Tel: 612-625-7219

```



DB	A75	GATGCTTTTTCAGACGCCTTGCAANGTTACGTTTTGGCAAAATCCGATTACTAATAAGC	531
RESULT	5		
LOCUS	AM329834		
DEFINITION	AM329834	548 bp mRNA	EST
ACCESSION	N201110E	rootphos(?) Medicago truncatula cDNA clone MHRP-24F8,	mRNA
VERSION	AM329834		
KEYWORDS	GI:7676124		
SOURCE	EST.		
ORGANISM	barrel medic.		
REFERENCE	Medicago truncatula		
AUTHORS	Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta; Magnoliophyta: eudicotyledons: core eudicots: Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.		
TITLE	1 (bases 1 to 548)		
JOURNAL	Harrison,M.J., Liu,J., Harris,A.R., Scott,A.D., Gonzales,R.A., Gonzales,M.B., and Ellis,L.		
COMMENT	ESTs from phosphate starved roots Unpublished (1999) On Jan 28, 2000 this sequence version replaced gi:6600429.		
	Contact: Harrison M.J.		
	Plant Biology Division		
	The Samuel Roberts Noble Foundation		
	2510 Sam Noble Parkway, Ardmore, OK 73401		
	Tel: 580-223-5810		
	Fax: 580-221-7380		
	Email: mjharrison@noble.org		
	Date: 1/23/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at 'http://chrystle.tamu.edu/Medicago'.		
	Seq primer: T3.		

FEATURES	SOURCE
location/Qualifiers	1. 548
/organism="Medicago truncatula"	
/cultivar="Jemalong, line A17"	
/db_xref="taxon:3880"	
/clone_id="MHRP-24F8"	
/clone_id="rootphos (-)"	
/tissue_type="roots"	
/dev_stage="phosphate starved"	
/note="vector: pluscript SK -; Site_1: EcoRI, Site_2: XhoI; At the trifoliolate stage, M. truncatula plants were transplanted to phosphate-free sand and grown for a further 30 days. During this 30 day period, they were fertilized twice weekly with 1/2 Hoaglands solution containing only 20uM potassium phosphate. RNA was prepared from the roots. cDNA was directionally ligated into the Uniap XR vector from Stratagene and packaged using GigaPack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-zap phage using Ex-assist helper phage and propagated in SOLR cells."	163 a 92 c 125 g 168 t

Query Match	34.4%	Score 165	DB 21	Length 548
Best Local Similarity	60.6%	Pred. No. 6.4e-38		
Matches 289	Conservative 0	Mismatches 185	Indels 3	Gaps 1
Qy 1	ggtgtttaaattatgaacgcagacacacccctgttataccagcagctcgcagctgttaag	60		
Db 53	GGTGCTTCAACTTTGAGAGATGAACCAACATCTATTGTAGTCCGCTAGACTTTACAA	112		
Qy 61	gccttataccttgatgacgaataacctcttccaaagtlgcaccccaagcattagcagt	120		
Db 113	GCTTTAGTTACAGATTCGTGATTAACCTTATCCCGAAGGTTATTG--ATGCATCCAAAGT	169		
Qy 121	gttgaacaactgaaggaatgaggggcctctgaacaccttaagaagaatcagctttccgaa	180		
Db 170	ATTGAATTTGTTGAAGGAACGCGTGGCCCGGAACATCAAGAAGAACTTATCGTTTAA	229		

QY 181 ggccctcccttcgaagtcagctgaagacagagctgaatgaagtcgagccacacaaatccaa 240  
Db 230 GGTCGTGAACAACAAGTATGATTTCCACAAAGTCAGCTTAGATGATGATTTAACTTTC 289  
QY 241 tacatctacagcgcgatcgaagggcggtcccaatgagcacacatctggagaagatctccaa 300  
Db 290 TACAACTCAGCATAGTTGGTGGTGGTGACTTCCAAACAGGGGAAAGATCTCTTT 349  
QY 301 gagataaagatagtcgacaacccctgatgagagatccatcttgaagatcagacaaatcac 360  
Db 350 GAGTCTAAATGTCGTCCAGGGCCAGATGAGACATTCATTCCAAAGCTTACTGTGAATAC 409  
QY 361 cacaccaagctgacatgaagtcgaagcagagcaggttaagcgaagtaagaatggc 420  
Db 410 TTCACCAAAAGGTGATGCTGCACCTAGTCGAAGAAGCAAAATCAAGGGTGGAAAAAGCTAGGGT 469  
QY 421 gagacactcttgaagcgctgtgagagctaacctcttgcaacatccagctgcctcaaac 477  
Db 470 GATGGTCTTTTCAAGGCTCTTGAAAGCTTACTCTTTTGGCAAACTCTGATTTCTAAGC 526

REFERENCE	AUTHORS	ORGANISM	ACCESSION	VERSION	KEYWORDS	DEFINITION	LOCUS	RESULT
BE203167			BE203167	627 bp	mRNA	EST	27-JUN-2000	
EST#403189	KVI	Medicago truncatula	cdna	clone	pKV1-4NL	mRNA		
sequence.								
BE203167			BE203167	GI:8746438				
EST.								
barrel medic.								
Medicago truncatula								
Eunariophyta; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;								
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;								
Fabales; Fabaceae; Papilionoideae; Medicago.								
1 (bases 1 to 627)								
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and								
Fraser,C.M.								
ESTs from roots of Medicago truncatula after Rhizobium inoculation								
Unpublished (1999)								
Contact: Vandenbosch K								
Department of Biology								
Texas A&M University								
College Station, TX 77843-3258, USA								
Tel: 409 845 7707								
Fax: 409 845 2891								
Email: kate@mail.bio.tamu.edu								
Texas A&M University:T262939e								
TIGR sequence name:MTIAK73M								
More information is available at.								
http://chryslie.tamu.edu/medicago								
Seg primer: SKmod (CTA gAA CTA gTg gAT CC).								

FEATURES	SOURCE
location/Qualifiers	1. 627
/organism="Medicago truncatula"	
/cultivar="genotype A17"	
/db_xref="taxon:3880"	
/clone="PKV1-4N1"	
/clone_1lb="KV1"	
/tissue_type="Seedling roots"	
/dev_stage="24 hours post-inoculation with Sinorhizobium	
melliotti AB57M"	
/lab_host="E. coli strain SOLR"	
/note="Vector: pBluescript SK -; Site.1: EcoRI; Site.2:	
XhoI; cDNA was prepared from polyA+ enriched RNA. The	
cDNA was directionally ligated into the unizap XR vector	
from Stratagene and packaged using GigaPack III gold	
packaging extracts. Plasmids containing cDNA inserts	
were excised from the recombinant lambda-zap phage using	
Ex-assist helper phage and propagated in SOLR cells."	
BASE COUNT	174 a
ORIGIN	100 c 147 g 206 t

Query Match	34.4%	Score 165;	DB 34;	Length 627;
Best Local Similarity	60.6%;	Pred. No. 6.6e-38;		
Matches 289;	Conservative 0;	Mismatches 185;	Indels 3;	Gaps 1

OY	1	ggtgtgttaataataagaagctgagaccacactcgttatacccaagcagcagctgagcttcaag	60
Db	16	GGTGCTTCAACTTGGAGGATGAACCAACATCTATTGTGCTCCTCCTGACTTTCANAA	75
OY	61	gcccttatcccttgatgycgataacctcttctccaaaggtgycacccccaagccattagagt	120
Db	76	GCTTATGTTACAGATTCCTATTAACCTTTATCCGGAAGGTTATTG---ATGCCATCCAAAT	132
OY	121	gttgaagaacattggaaggaatgtgagggccttggaaccattaaagaatctgcgttcccgaa	180
Db	133	ATTGAAATTTGTTGAAGGAAACGCTGGCGGGAACCATCAAGAAACCTTACTTTGTTGAA	192
OY	181	ggcctcccttccaagtagcagaagcagagcttgatgtaggtgagccacacaaacttcaaa	240
Db	193	GGTGGTGAAACAAAGATATATTTCACCAAAAGTGGAATTTAGTAGATATGTTAACTTTGCT	252
OY	241	tacaattacagcgtgatacgaagggcgtgccataagcgcagacacattggaagaatctccaac	300
Db	253	TACAACCTACAGCATGTGTTGGTGGTGACATTCACAGACACAGCTGGAGAGAATCTCTCTT	312
OY	301	gagatlaaagatgtgccaacccctgatagtgaagatccatcttgaagtgtcgaacaagtgc	360
Db	313	CAGTCTAAATTTCTGCAAGGGCCAGATGGAAGATTCATTCGCAAAAGCTTACTGTGAATATC	372
OY	361	cacaccaaagtgacatcgaatgaagtgaaagcagcagtgtaagtcgaagtaagaatagggc	420
Db	373	TTTACCAAAAGGATGTCCTCACCTAGTGAAGAGAAATCAAGGTCGGAANAAGCTAGGGGT	432
OY	421	gagacacttttgaggccgttgtagagctaccctcttggcacacttcgaatgctctacaac	477
Db	433	GATGTCCTTTTTCAAAGGCTCTTGAAGGTTACGTTTGGCAAAATCCTATTTACCTAAAC	489

RESULT	7			
LOCUS	AM686778			
DEFINITION	AM686778	643 bp	mRNA	EST 15-JUN-2000
ACCESSION	NF042608NR1F1000	Modulated root Medicago truncatula cDNA clone		
VERSION	NF042608NR.5	mRNA sequence.		
KEYWORDS	AM686778			
SOURCE	AM686778.1	GI:7561514	EST.	
ORGANISM	barrel medic.			
REFERENCE	Medicago truncatula			
AUTHORS	Eunaxyfolia, Viridiplantae; Embryophyta; Tracheophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Medicago.			
	1 (bases 1 to 643)			
	Watson,R.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.T., Flores,H.R., Inman,J.T., Weller,J.W., May			
	,G.D. and Palva,N.L.			
TITLE	Expressed Sequence Tags from the Samuel Roberts Noble Foundation			
JOURNAL	Medicago truncatula modulated root library			
COMMENT	Unpublished (2000)			
	Contact: Palva NL			
	Plant Biology Division			
	The Samuel Roberts Noble Foundation			
	2510 Sam Noble Parkway, Ardmore, OK 73402, USA			
	Tel: 580 221 7317			
	Fax: 580 221 7380			
	Email: nl.palva@noble.org			
	Insert Length: 643	Std Error: 0.00		
	Plate: 042	row: G	column: 08	
FEATURES	Seq primer: TCACACAGGAACACGCTATGAC.			
	location/Qualifiers			
	1..643			
	/organism="Medicago truncatula"			
	/db_xref="taxon:3880"			

BASE COUNT	ORIGIN
185 a	102 c 143 g 213 t

Query Match	34.4%	Score 165;	DB 23;	Length 643;
Best Local Similarity	60.6%	Pred. No. 6.7e-38;		
Matches 289; Conservative	0;	Mismatches 185;	Indels 3;	Gaps 1;

[illegible]

RESULT	8
BE203464	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	

BE203464 661 bp mRNA EST 27-JUN-2000  
 EST403466 KVI Medicago truncatula cDNA clone pkvi-5L19, mRNA  
 sequence.  
 BE203464  
 BE203464.1 GI:8746737  
 EST.  
 barrel medic.  
 Medicago truncatula  
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta  
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 Fabales; Fabaceae; Papilionoideae; Medicago.  
 1 (bases 1 to 661)  
 VandenBosch,K., Hurt,J., Moore,J., Beremand,P., Peng,H., Ellis,L.,  
 Town,C.P., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and  
 Fraser,C.M.  
 ESTs from roots of Medicago truncatula after Rhizobium inoculation  
 Unpublished (1999)  
 Contact: VandenBosch K  
 Department of Biology  
 Texas A&M University  
 College Station, TX 77843-3258, USA  
 Tel: 409 845 7707  
 Fax: 409 845 2891



Db 341 GAGTCAATTTCTGTCAGAGGCCAGATGAGATCCATTGCAAACTTACTGTGAATAC 400  
 QY 361 cacaccaaaagtgaccatgagtggaagcagagcaagtaagcaagtaagaatgagc 420  
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 Db 401 TTCACCAAGGTATGCTGACCTAGTGAAGAGGAAATCAAGGGGTGAAGGCTAGGGGT 460  
 QY 421 gagacactttgagggccgttgagagacactcttgagacactcgcagatgcataac 477  
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 Db 461 GATGCTTTTCAAGGCTTGAAGGTTAGCTTTGGCAAACTCTGATTACTTAAGC 517

RESULT 10  
 AM755334 540 bp mRNA EST 03-MAY-2000  
 LOCUS s101902.X1 GM-cl036 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:  
 DEFINITION GM-cl036-75 5' similar to FR:P93330 P93330 MN13 GENE. ;, mRNA  
 sequence.  
 ACCESSION AM755334  
 VERSION AM755334 GI:7684686  
 KEYWORDS EST.  
 SOURCE soybean.  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 Fabales; Fabaceae; Papilionoideae; Glycine.  
 1 (bases 1 to 540)  
 Shoemaker, R., Kelm, P., Vodkin, L., Erpelding, J., Correll, V., Khanna,  
 A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,  
 Wylie, T., Underwood, K., Stepien, M., Theising, B., Allen, M., Bowers,  
 Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Hallen, N., Schurk,  
 R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann,  
 R., Waterston, R. and Wilson, R.  
 Public Soybean EST Project  
 Unpublished (1999)  
 Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.edu  
 This clone is available through: Genome Systems, Inc. 4633 World  
 Parkway Circle St. Louis, Missouri 63134 For further information  
 call: (800) 430-0030 or (314) 427-3222 FAX: (888) 919-3324 or (314)  
 427-3334 or contact: clones@genomesystems.com or  
 info@genomesystems.com web site: www.genomesystems.com  
 High quality sequence stop: 435.  
 Location/Qualifiers  
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 /db\_xref="taxon:3847"  
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 /clone\_1lb="GM-cl036"  
 /rname\_type="somatic embryos cultured on MSD 20"  
 /lab\_host="DH10B"  
 /note="Vector: pSPORT1; Site\_1: NotI; Site\_2: SalI; This  
 cDNA library was constructed from mRNA isolated from  
 somatic embryos (age ranging from 2 months to 9 months)  
 cultured on MSD 20. The library was prepared using the  
 Life Technologies pSuperScript cDNA library construction  
 kit. Complementary DNA was synthesized from mRNA using a  
 poly (dT) sequence with a NotI restriction site. SalI  
 linkers adapters were ligated to the blunt-ended cDNA  
 fragments followed by NotI digestion. The cDNA fragments  
 were directionally cloned into the NotI-SalI restriction  
 site of the pSPORT1 vector. The ligated cDNA fragments  
 were transformed into E.coli Electromax DH10B host cells.  
 This library was constructed in the laboratory of Dr. Lila  
 Vodkin by Anu Khanna at the University of Illinois at  
 Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"

BASE COUNT 167 a 100 c 116 g 156 t 1 others  
 ORIGIN

Query Match 34.3%; Score 164.6; DB 24; Length 540;  
 Best Local Similarity 60.8%; Pred. No. 8.3e-38;  
 Matches 288; Conservative 0; Mismatches 180; Indels 6; Gaps 1;

QY 1 ggtgtttaattaatgagactgagaccactctgttaaccgaagctcagatgttcaag 60  
 Db 73 GGTGTTTTCACCTTGTGAAGGAAACAGCTTTCCCGCTCTGTGTGCAAAATATACAA 132  
 QY 61 gcccttaaccttgatggcgataacctcttccaaaggttgaccccaagcattagcag 120  
 Db 133 GCTATTGCTCTAGATGCGACCAAGTCTTCCCAAAACCATTTGCCAATTTCAATAGAGC 192  
 QY 121 gttgaacacttgagaaatggagggccctgggaacacttaagaagatcagctccgaa 180  
 Db 193 GTAGAAACCATTTGAAGAGATGAGAGGCCAGGAACCTTAAGAAGCTTACTTGTGTGA 252  
 QY 181 ggcctcccttcaagtaagtcgtaagagacagatgtgatggatggagacacaaactcaaa 240  
 Db 253 GG-----TTTAGGTTATGTGAAGCACACGTCATGATGCAATTCACAGAAACTATGTG 306  
 QY 241 tacataacagcgtgatcgagggcggtcccatagggagacacattgagaagatctccaac 300  
 Db 307 TACACATATAGTGTGATGGAAGGCGATGTCGAGACCATTTGAGATATGTAT 366  
 QY 301 gagataagataatggagacccccctgatggagagatccatcttgagatcagcaacagatc 360  
 Db 367 GAGTACCAACTGATGGCGACACCCAGATGAGAGATCCATTGTGAAGTCCACACCAATATAC 426  
 QY 361 cacaccaaaagtgaccatgagtggaagcagagcaagtaagcaagtaagaatgagc 420  
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 Db 427 TATACCAAGGTGATGAGCAACTCGNCGAAATATGTGAAGACTGGCAGAGAGATGC 486  
 QY 421 gagacactttgagggccgttgagagactaccttgagacactcgcagatgcctac 474  
 Db 487 GCAGGTTTCAACCAAGGCTATTGAGATTCATTGAGGCTAATCTGATTATCAAC 540

RESULT 11  
 AV428823 541 bp mRNA EST 02-MAY-2000  
 LOCUS AV428823 lotus japonicus young plants (two-week old) Lotus  
 DEFINITION japonicus cDNA clone MM073a12\_r 5', mRNA sequence.  
 ACCESSION AV428823  
 VERSION AV428823.1 GI:7678205  
 KEYWORDS EST.  
 SOURCE Lotus japonicus.  
 ORGANISM Lotus japonicus  
 Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;  
 Fabales; Fabaceae; Papilionoideae; Lotus.  
 1 (bases 1 to 541)  
 Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
 Generation of 7137 non-redundant expressed sequence tags from a  
 legume, Lotus japonicus  
 DNA Res. 7 (2), 127-130 (2000)  
 20277479  
 JOURNAL MEDLINE  
 COMMENT The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yana 1532-3, Kisarazu, Chiba 252-0812, Japan  
 Email: asamizu@kazusa.or.jp; URL: http://www.kazusa.or.jp/en/plant/  
 Location/Qualifiers  
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 /clone="MM073a12\_r"  
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 /dev\_stage="young plants (two-week old)"  
 /note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2:  
 XhoI; Isolate=MIYAKOJima MG-20"

BASE COUNT 158 a 120 c 113 g 150 t  
 ORIGIN



info@genomesystems.com web site: [www.genomesystems.com](http://www.genomesystems.com)  
 High quality sequence stop: 420.  
 Location/Qualifiers  
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 /organism="Glycine max"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-c1028-6568"  
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 /tissue\_type="roots of 'Supernod' plants"  
 /lab\_host="DHI0B"  
 /note="Vector: pBluescript II XR; Site\_1: EcoRI; Site\_2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicus, strain USDA110 prior to harvest. Stratagene's cDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dcmp, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A-C, or G) was added to the 3' end of the primer (GAGAGAGAGAGAGAGAGAGACATGCTGAGCTT)18V to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GibcoBRL Life Technologies' cDNA Size Fractionation column. The column eluent was then ligated into Stratagene's pBluescript II XR predigested vector (pBluescript II SK+) that has been digested with EcoRI and XhoI, and phosphorylated by Stratagene). Both the white and blue colonies appear to contain recombinant plasmids with cDNA inserts, based on size (n=25). This library was constructed by Dr. Paul Keim and Dr. Virginia Coryell."

BASE COUNT 157 a 94 c 114 g 118 t  
 ORIGIN  
 Query Match 34.2%; Score 164; DB 32; Length 483;  
 Best Local Similarity 60.8%; Pred. No. 1.2e-37;  
 Matches 288; Conservative 0; Mismatches 180; Indels 6; Gaps 1.

QY 1 ggtgtgttaattatgagactgagacacactgttatccagcagctcgactgttcaag 60  
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 Db 16 GGTGTTTTCACCTTCGAAAGGGAACCCCTTCCCGCTGCTGCAAAATTAACAA 75  
 QY 61 gccattacccttgataggagataactcctttccaaggtgtcaaccccaagcattgagct 120  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 76 GCTATTGTCTAGAGATCCAGCAATGCTTTCCCAAAGCATTTGCCAAATTTCTTAAGAGC 135  
 QY 121 gttgaanaacattgaaagaaatcgagaggtcgtgaaacattaaagaagaatcagcttccgaa 180  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 136 GTAGAAACCATTTGAAAGAGATGAGAGGCGCAGGAACATTAGAAACCTTACTTCTCTGAA 195  
 QY 181 ggctcccttccaagtacggtgaagacagagttgatsaggtgagaccacacaaacttcaaa 240  
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 Db 196 GG-----TTTAGGTATTAGTGAAGCACCACGTAGTCAATTAACACAGAAAACTATGTG 249  
 QY 241 tacaattcacagcgtgatcgtgaaggcggttccataagcgcagacattggaagaatctccaac 300  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 250 TACAACCTTATAGTGTGATTGGAAGCGCATGTCATTGTCGGACCATTTGGAAGATTAAGTTAT 309  
 QY 301 gagataaagatagtggaacccctgatgagagatccatcttgaagaatcagacaagatc 360  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
 Db 310 GAGTACAAACTGTGTGGCAACCCAGATGAGAGATCCATTGTGAACTCCACAAGCAAAATAC 369  
 QY 361 cacaccnaagtgaccatgaggtgaaaggcagacaggttlaaggtcgaagttaagaagtggc 420  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db	370	TATACCAAGGNGAGGACCACTCGGCCGAAGAATATGTGAACATCGGCAAGGAGATCT	429
Oy	421	gagacactcttgaggcgcttgaagactcctcttgacactccgatgcctac	474
Db	430	GCAGGTTTCACCAAGGCTATTGAGGATTTCAATTCAGGCTAAATCTGATTACAC	483
RESULT 13			
AM234941			
LOCUS	AM234941	498 bp	EST
DEFINITION	s121a03.y1 Gm-cl028 Glycine max cDNA clone		17-JUL-2000
VERSION	Gm-cl028-581 5'	similar to SW:SA42_SOYBN P26987	GENOME SYSTEMS CLONE ID:
KEYWORDS	PROTEIN SAM22. ; mRNA sequence.		STRESS-INDUCED
ACCESSION	AM234941		
VERSION	AM234941.1	GI:6567330	
KEYWORDS	EST.		
SOURCE	soybean.		
ORGANISM	Glycine max		
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids 1; Fabales; Fabaceae; Papilionoideae; Glycine.		
AUTHORS	1 (bases 1 to 498) Shoemaker,R., Kelm,P., Vodka,L., Expediting,J., Corvelli,V., Khanna,A., Bolla,B., Marr,P.M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,T., Persson,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr,R., Ritter,E., Kohn,S., Shih,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R. Public Soybean EST Project Unpublished (1999) Contact: Shoemaker R/Public soybean EST project Public Soybean EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: est@wustl.wustl.edu This clone is available through: Genome Systems, Inc. 4633 World Parkway Circle St. Louis, Missouri 63134 For further information call: (800) 430-0030 or (314) 427-3322 FAX:(888) 919-3324 or (314) 427-3324 or contact: clones@genomesystems.com or info@genomesystems.com web site: www.genomesystems.com Insert length: 940 Std Error: 0.00 High quality sequence stop: 430.		
TITLE			
JOURNAL			
COMMENT			
FEATURES			
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	/db_xref="taxon:3847"		
	/clone="GENOME SYSTEMS CLONE ID: Gm-cl028-581"		
	/clone_lib="Gm-cl028"		
	/tissue_type="roots of 'Supernod' plants"		
	/lab_host="DH10B"		
	/note="Vector: pBluescript II XR; Site:1: EcoRI; Site:2: XhoI; The mRNA was isolated from roots of Glycine max 'Supernod' plants generously donated by Dr. Gary Stacey. The seedlings were inoculated with Bradyrhizobium japonicus, strain USDA110 prior to harvest. Stratagene's cDNA synthesis kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dcmp, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V-A, C, or G) was added to the 3' end of the primer [GACACGACGACGACGACGACGACGACGACGAG(T)18V] to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA polymerase, ligated to EcoRI adapters and subsequently phosphorylated. The XhoI site within the first-strand synthesis primer was then restricted by digestion with XhoI; all XhoI sites in the cDNA would be protected by their hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using GlibcoobRL Life Technologies' cDNA Size Fractionation		

BASE COUNT	144 a	117 c	121 g	116 t
Query Match	34 1%	Score 163.6;	DB 20;	Length 498;
Best Local Similarity	60.5%;	Pred. No. 1.6e-37;		
Matches 287;	Conservative	0;	Mismatches 184;	Indels 3;
				Gaps 1;
Column. The column eluent was then ligated into				
Stratagene's Bluescript II XR Predigested Vector				
(pBluescript II SK(+)) that has been digested with				
EcoRI and XhoI, and phosphorylated by Stratagene). Both the				
white and blue colonies appear to contain recombinant				
plasmids with cDNA inserts, based on size (0.25). This				
library was constructed by Dr. Paul Keim and Dr. Virginia				
Coryell."				
1 ggtgtgttaataatgaagactgaagacacactctgtatccagcagctgactgttcaag 60				
28 GGTGTTTACATTCAGATCCGACAAACGTCAATCCAAAGGCT---CTTGATTCCTTCAAGT 144				
61 gccctatcccttgaagcagataacctcttccaaagtgtcaccccaagcattagcagt 120				
88 GCGCTAGTACAGATCCGACAAACGTCAATCCAAAGGCT---CTTGATTCCTTCAAGT 144				
121 gttaagaacattgaagaaatggaagggcctgtgaaccattagaagaatcagcttccgaa 180				
145 GTTGAAGAAAGTTGAGGGAATGTGTGCCCGCAGAACCATCAAGATCACTTCTCTTGAG 204				
181 ggcctcccttcaatgaagcagtgaaagcagaatttgaaggtgagcaccacaacttcaaa 240				
205 GATGAGAAACCAAGTTTGTCTGCCAATAATGAAAGCATGATGAGCGCAATTTGGCA 264				
241 taacaattacagcgtgacgcgagggcgttcccatagagcagacacattggaagaatccaac 300				
265 TACAGCTACAGCGTGGTGGGGGTGCTGATTCGCCAGACACGCGGAGAAATCAATTC 324				
301 gagataaagatagtggcaacccctgatgtgaagatccatttgaagatacgaacaagtac 360				
325 GATCCAAATTTGGTCTGTCTGCCAATGAGGAGTCTGCTGGAGCACTCACTGTCAATATTC 384				
361 caacccaagaagtcgacatgagtgtaagcagaagcaggttaagcagaatgaagaatggac 420				
385 GAAACAAAAGAGATGCTCTGACGCCCAACAGACGAACCTAAATACGTGGAAGAACCAAGCT 444				
421 gagaacatttgaagggcgttgaagactcaactcttggcaactccgagtccac 474				
445 GATGCTCTCTTCAAGGCCCATGTAGGGCTTACCTTTGGCCCATCCGATTACAC 498				
RESULT 14				
LOCUS A1988606 507 bp mRNA EST 17-JUL-2000				
DEFINITION sds5a12.y1 Gm-cl020 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl020-791.5' similar to SW:SAM2_S0YEN P26987 STRESS-INDUCED				
PROTEIN SAM22.; mRNA sequence.				
ACCESSION A1988606				
VERSION A1988606.1 GI:5820400				
KEYWORDS EST.				
SOURCE soybean.				
ORGANISM Glycine max				
REFERENCE Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.				
AUTHORS 1 (bases 1 to 507)				
Shoemaker, R., Keim, P., Vodkin, L., Erpelde, J., Coryell, V., Khanna, A., Bolla, B., Maria, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Mattern, R., and Wilson, R.				
TITLE Public soybean EST Project				
COMMENT Unpublished (1999)				
CONTACT Shoemaker R/Public Soybean EST Project				



